

#2
OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/837,961

DATE: 05/08/2001
 TIME: 15:59:31

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 Output Set: N:\CRF3\05082001\I837961.raw

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3 <110> APPLICANT: Payne, Jewel
4      Sick, August
6 <120> TITLE OF INVENTION: Novel Bacillus thuringiensis Isolate Active Against Lepidopteran Pests,
7      and Genes Encoding Novel Lepidopteran-Active Toxins
9 <130> FILE REFERENCE: MA-43CDF2D3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/837,961
C--> 11 <141> CURRENT FILING DATE: 2001-04-19
11 <150> PRIOR APPLICATION NUMBER: US 09/521,344
12 <151> PRIOR FILING DATE: 2000-03-09
14 <150> PRIOR APPLICATION NUMBER: US 08/933,891
15 <151> PRIOR FILING DATE: 1997-09-19
17 <150> PRIOR APPLICATION NUMBER: US 08/356,034
18 <151> PRIOR FILING DATE: 1994-12-14
20 <150> PRIOR APPLICATION NUMBER: US 08/210,110
21 <151> PRIOR FILING DATE: 1994-03-17
23 <150> PRIOR APPLICATION NUMBER: US 07/865,168
24 <151> PRIOR FILING DATE: 1992-04-09
26 <150> PRIOR APPLICATION NUMBER: US 07/451,261
27 <151> PRIOR FILING DATE: 1989-12-14
29 <150> PRIOR APPLICATION NUMBER: US 371,955
30 <151> PRIOR FILING DATE: 1989-06-27
32 <160> NUMBER OF SEQ ID NOS: 8
34 <170> SOFTWARE: PatentIn version 3.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 3528
38 <212> TYPE: DNA
39 <213> ORGANISM: Bacillus thuringiensis
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46 caatttctgt tgagtgaatt tgtcccagggt gctgggttt tattaggttt aattgattta    180
48 atatgggggt ttgtgggtcc ctctcaatgg gatgcatttc ttgtgcaaat tgaacaggtta    240
50 attaacccaa gaatagagga attcgctagg aaccaagcaa tttctagatt agaaggggcta    300
52 agcaaccttt atcaaattta cgcagaagct ttttagagagt gggaaagcaga tcctactaat    360
54 ccagcattaa cagaagagat gcttattcgt ttcaatgaca tgaacagtgc tcttacaacc    420
56 gctattcctc ttttacagt tcaaaattat caagtacctc ttctatcagt atatgttcaa    480
58 gctgcaaatt tacatttata ggttttgaga gatgtttcag tggggaca acgttgggga    540
60 tttgatgtag caacaatcaa tagtcgttat aatgatttaa ctaggcttat tggcacctat    600
62 acagattatg ctgtacgctg gtataatcgt ggattagaac gtgtatgggg accggattct    660
64 agagattggg taaggatataa tcaatttaga agagagctaa cactaactgt attagatatc    720
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70 gctcagagaa tagaacagaaa tattaggcaa ccacatctta tggatctctt taatagtata    900
72 accatttata ctgatgtgca tagaggcttt aattatttgtt caggacatca aataacagct    960
74 tctctgtcg gttttgcggg gccagaattt actttccta gatatggAAC catggaaat    1020
76 gctgctccac ccgtactgtat ctcaactact ggtttggga tttttagaac attatctca    1080
78 cctcttaca gaagaattat acttggttca ggcggaaata atcagaacct gtttgcctt    1140

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86	gttacacct	tgagagctcc	aacgtttct	tggcgacatc	gtagtgtca	attctctaAC	1380										
88	ctaattccTTT	catcacAAAT	cacacagata	cctttaacaa	agtctattaa	tcttggctct	1440										
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94	gtaagaattc	gctacgcttc	tactacAAAT	ttacaattcc	atacatcaat	tgacggaaga	1620										
96	cctattaATC	aggggaattt	ttcagcaact	atgagtagtg	ggggtaattt	acagtccggA	1680										
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112	gatattacca	tccaaaggagg	agatgacgta	ttcaaagaga	attacgtcac	actaccgggt	2160										
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120	ccgcTTTCAG	tgcAAAATCC	aatttggaaAG	tgcggagaAC	caaATcgatG	cgcaccacAA	2400										
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126	gtatGGGTGA	tattcaAAAT	taagatgca	gatggtcacg	caagactagg	taatctagag	2580										
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140	aatGGCTTAT	catgctgaa	cgtGAAAGGG	catgttagatG	tagaagaaca	aaacaaccac	3000										
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152	tccatACCAg	ctgagatATGC	gccagTTTAT	gaggaAGCAT	atatGATGG	aagaaaaAGAG	3360										
154	aatcCTTGTG	aatctaACAG	aggatATGGG	gattacacgc	cactaccAGC	tggttatgt	3420										
156	acaaaAGAAAT	tagatGACTT	cccAGAAACC	gataaggat	ggattgagat	cggggaaACG	3480										
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171	Thr	Ile	Glu	Ile	LLe	Glu	Gly	Glu	Arg	Ile	Glu	Thr	Gly	Tyr	Thr	Pro	
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174 Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser Glu Phe Val
 175 35 40 45
 177 Pro Gly Ala Gly Phe Val Leu Gly Leu Ile Asp Leu Ile Trp Gly Phe
 178 50 55 60
 180 Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln Leu
 181 65 70 75 80
 183 Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg
 184 85 90 95
 186 Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu Ala Phe Arg
 187 100 105 110
 189 Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Thr Glu Glu Met Arg
 190 115 120 125
 192 Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu
 193 130 135 140
 195 Phe Thr Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val Tyr Val Gln
 196 145 150 155 160
 198 Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe Gly
 199 165 170 175
 201 Gln Arg Trp Gly Phe Asp Val Ala Thr Ile Asn Ser Arg Tyr Asn Asp
 202 180 185 190
 204 Leu Thr Arg Leu Ile Gly Thr Tyr Asp Tyr Ala Val Arg Trp Tyr
 205 195 200 205
 207 Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg Asp Trp Val
 208 210 215 220
 210 Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val Leu Asp Ile
 211 225 230 235 240
 213 Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro Ile Arg Thr
 214 245 250 255
 216 Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val Leu Glu Asn
 217 260 265 270
 219 Phe Asp Gly Ser Phe Arg Gly Met Ala Gln Arg Ile Glu Gln Asn Ile
 220 275 280 285
 222 Arg Gln Pro His Leu Met Asp Leu Leu Asn Ser Ile Thr Ile Tyr Thr
 223 290 295 300
 225 Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln Ile Thr Ala
 226 305 310 315 320
 228 Ser Pro Val Gly Phe Ala Gly Pro Glu Phe Thr Phe Pro Arg Tyr Gly
 229 325 330 335
 231 Thr Met Gly Asn Ala Ala Pro Pro Val Leu Ile Ser Thr Thr Gly Leu
 232 340 345 350
 234 Gly Ile Phe Arg Thr Leu Ser Ser Pro Leu Tyr Arg Arg Ile Ile Leu
 235 355 360 365
 237 Gly Ser Gly Pro Asn Asn Gln Asn Leu Phe Val Leu Asp Gly Thr Glu
 238 370 375 380
 240 Phe Ser Phe Ala Ser Leu Thr Ala Asp Leu Pro Ser Thr Ile Tyr Arg
 241 385 390 395 400
 243 Gln Arg Gly Thr Val Asp Ser Leu Asp Val Ile Pro Pro Gln Asp Asn
 244 405 410 415
 246 Ser Val Pro Ala Arg Ala Gly Phe Ser His Arg Leu Ser His Val Thr

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252	Phe Ser Trp Arg His Arg Ser Ala Glu Phe Ser Asn Leu Ile Pro Ser		
253	450	455	460
255	Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Ile Asn Leu Gly Ser		
256	465	470	475
258	Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		
259	485	490	495
261	Arg Ile Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val Thr Ile Thr		
262	500	505	510
264	Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr		
265	515	520	525
267	Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln		
268	530	535	540
270	Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Gly Asn Leu Gln Ser Gly		
271	545	550	555
273	Ser Phe Arg Thr Ala Gly Phe Thr Thr Pro Phe Asn Phe Ser Asn Gly		
274	565	570	575
276	Ser Ser Ile Phe Thr Leu Ser Ala His Val Phe Asn Ser Gly Asn Glu		
277	580	585	590
279	Val Tyr Ile Glu Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu		
280	595	600	605
282	Ala Glu Tyr Asp Leu Glu Arg Ala Gln Glu Ala Val Asn Ala Leu Phe		
283	610	615	620
285	Thr Ser Ser Asn Gln Leu Gly Leu Lys Thr Asn Val Thr Asp Tyr His		
286	625	630	635
288	Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Gly Glu Phe Cys		
289	645	650	655
291	Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Asn Arg		
292	660	665	670
294	Leu Ser Asp Glu Arg Asn Leu Gln Asp Pro Asn Phe Arg Gly Ile		
295	675	680	685
297	Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile		
298	690	695	700
300	Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly		
301	705	710	715
303	Thr Phe Asn Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu		
304	725	730	735
306	Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu		
307	740	745	750
309	Asp Ser Gln His Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Thr Lys His		
310	755	760	765
312	Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Val		
313	770	775	780
315	Glu Asn Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro Gln		
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321 Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Ile Gly Cys
 322 820 825 830
 324 Thr Asp Leu Asn Glu Asn Leu Gly Val Trp Val Ile Phe Lys Ile Lys
 325 835 840 845
 327 Met Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
 328 850 855 860
 330 Lys Pro Leu Val Gly Glu Ser Leu Ala Arg Val Lys Arg Ala Glu Lys
 331 865 870 875 880
 333 Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Val Glu Thr Asn Ile Val
 334 885 890 895
 336 Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
 337 900 905 910
 339 Tyr Asp Arg Leu Gln Ala Asp Thr Asp Ile Ala Met Ile His Ala Ala
 340 915 920 925
 342 Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
 343 930 935 940
 345 Val Ile Pro Gly Val Asn Ala Gly Ile Phe Glu Glu Leu Glu Gly Arg
 346 945 950 955 960
 348 Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
 349 965 970 975
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 352 980 985 990
 354 Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu
 355 995 1000 1005
 357 Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
 358 1010 1015 1020
 360 Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu
 361 1025 1030 1035
 363 Gly Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu
 364 1040 1045 1050
 366 Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
 367 1055 1060 1065
 369 Val Thr Cys Asn Asp Tyr Thr Ala Asn Gln Glu Glu Tyr Gly Gly
 370 1070 1075 1080
 372 Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Gly Glu Ser Tyr Glu Ser
 373 1085 1090 1095
 375 Asn Ser Ser Ile Pro Ala Glu Tyr Ala Pro Val Tyr Glu Glu Ala
 376 1100 1105 1110
 378 Tyr Ile Asp Gly Arg Lys Glu Asn Pro Cys Glu Ser Asn Arg Gly
 379 1115 1120 1125
 381 Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu
 382 1130 1135 1140
 384 Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly
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VERIFICATION SUMMARY
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date